

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds

(without alignments)  
307.073 Million cell updates/sec

Title: US-09-940-860-1

Perfect score: 20

Sequence: 1.gcaaacagcagtagatcccc 20

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTCUTS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	20	100.0	24 3 US-09-073-465-9	Sequence 9, Appli
2	20	100.0	195 1 US-08-227-475-7	Sequence 7, Appli
3	20	100.0	279 4 US-09-107-532A-3170	Sequence 3170, Ap
4	20	100.0	279 4 US-09-107-532A-3171	Sequence 3171, Ap
5	20	100.0	538 3 US-08-979-566-3	Sequence 3, Appli
6	20	100.0	538 4 US-09-577-640-3	Sequence 3, Appli
7	20	100.0	571 3 US-09-328-111-755	Sequence 755, App
8	20	100.0	619 3 US-08-953-171-2	Sequence 2, Appli
9	20	100.0	624 3 US-09-328-111-728	Sequence 728, App
10	20	100.0	660 1 US-08-114-695A-5	Sequence 5, Appli
11	20	100.0	665 3 US-09-328-111-476	Sequence 476, App
12	20	100.0	672 3 US-09-328-111-450	Sequence 450, App
13	20	100.0	851 1 US-07-898-905-1	Sequence 1, Appli
14	20	100.0	851 1 US-07-898-905-2	Sequence 2, Appli
15	20	100.0	851 1 US-07-898-905-3	Sequence 3, Appli
16	20	100.0	851 3 US-09-006-089-1	Sequence 1, Appli
17	20	100.0	851 3 US-09-006-089-2	Sequence 2, Appli
18	20	100.0	851 3 US-09-006-089-3	Sequence 3, Appli
19	20	100.0	876 2 US-08-642-229A-4	Sequence 4, Appli
20	20	100.0	881 5 PCT-US91-01574-13	Sequence 13, Appli
21	20	100.0	882 2 US-07-923-871C-13	Sequence 13, Appli
22	20	100.0	1208 3 US-09-187-946-1	Sequence 1, Appli
23	20	100.0	1325 2 US-08-632-470-50	Sequence 50, Appli
24	20	100.0	1336 2 US-08-437-013-3	Sequence 3, Appli
25	20	100.0	1366 4 US-09-275-506A-3	Sequence 4, Appli
26	20	100.0	1366 4 US-09-191-099-4	Sequence 4, Appli
27	20	100.0	1385 4 US-09-735-567-1	Sequence 1, Appli

28	20	100.0	1396 3 US-08-953-171-6	Sequence 6, Appli
29	20	100.0	1400 4 US-09-375-932A-5	Sequence 5, Appli
30	20	100.0	1405 3 US-09-191-099-5	Sequence 5, Appli
31	20	100.0	1407 3 US-09-193-377B-2	Sequence 2, Appli
32	20	100.0	1407 4 US-09-517-744B-1	Sequence 1, Appli
33	20	100.0	1408 2 US-08-632-470-40	Sequence 40, Appli
34	20	100.0	1413 3 US-09-191-099-1	Sequence 1, Appli
35	20	100.0	1414 3 US-09-191-099-6	Sequence 6, Appli
36	20	100.0	1415 2 US-08-632-470-52	Sequence 52, Appli
37	20	100.0	1415 3 US-09-193-377B-9	Sequence 9, Appli
38	20	100.0	1417 4 US-09-191-099-2	Sequence 2, Appli
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42	20	100.0	1426 3 US-09-193-377B-7	Sequence 7, Appli
43	20	100.0	1427 2 US-08-632-470-27	Sequence 27, Appli
44	20	100.0	1428 3 US-09-193-377B-1	Sequence 1, Appli
45	20	100.0	1429 3 US-09-193-377B-8	Sequence 8, Appli

## ALIGNMENTS

RESULT 1  
US-09-073-465-9  
Sequence 9, Application US/09073465  
Patent No. 6054278  
GENERAL INFORMATION:  
APPLICANT: DODGE, Deborah E  
APPLICANT: SMITH, Doug  
TITLE OF INVENTION: RIBOSOMAL RNA GENE POLYMORPHISM BASED MICROORGANISM  
FILE REFERENCE: 4343 US  
CURRENT APPLICATION NUMBER: US/09/073,465  
CURRENT FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentm Ver. 2.1  
SEQ ID NO 9  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Bacterial  
US-09-073-465-9

Query Match 100.0%; Score 20; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAAACGAGTAGATACCC 20  
Db 2 GCAAAACGAGTAGATACCC 21  
RESULT 2  
US-08-227-475-7/c  
Sequence 7, Application US/08227475  
Patent No. 5571674  
GENERAL INFORMATION:  
APPLICANT: Hoshina, Sadayori  
APPLICANT: Weinstein, I. Bernard  
TITLE OF INVENTION: DNA Oligomers For Use In Detection Of  
TITLE OF INVENTION: Microorganisms And Methods Of Using Such DNA  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COOPER & DUNHAM  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds

(without alignments)  
307.073 Million cell updates/sec

Title: US-09-940-860-2  
Perfect score: 20  
Sequence: 1 ggaggaagcgagagatgacg 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 segs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: \*  
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3: /cgn2\_6/prodata/2/ina/6A COMB.seg: \*  
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6: /cgn2\_6/prodata/2/ina/backfile1.seg: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	100.0	2751	3 US-09-052-333A-6	Sequence 6, Appl
3	20	100.0	2752	3 US-09-052-333A-37	Sequence 37, Appl
4	20	100.0	1230025	4 US-09-198-452A-1	Sequence 1, Appl
5	16	80.0	420	4 US-09-252-991A-11029	Sequence 11029, A
6	16	80.0	1107	4 US-09-252-991A-13363	Sequence 13363, A
7	16	80.0	1179	4 US-09-252-991A-13193	Sequence 13193, A
8	16	80.0	1308	4 US-09-252-991A-12614	Sequence 12614, A
9	16	80.0	1683	4 US-09-252-991A-11226	Sequence 11226, A
10	16	80.0	1974	4 US-09-252-991A-11111	Sequence 11111, A
11	16	80.0	2283	4 US-09-252-991A-10956	Sequence 10956, A
12	15	75.0	191	4 US-09-621-976-8573	Sequence 8573, Ap
13	15	75.0	752	3 US-08-818-111-2	Sequence 2, Appl
14	15	75.0	752	4 US-08-818-111-2	Sequence 2, Appl
15	15	75.0	752	4 US-09-056-556-2	Sequence 2, Appl
16	15	75.0	752	4 US-09-072-596-2	Sequence 2, Appl
17	15	75.0	752	4 US-09-072-596-2	Sequence 2, Appl
18	15	75.0	889	4 US-09-050-739-5	Sequence 5, Appl
19	15	75.0	1245	4 US-09-252-991A-6286	Sequence 6286, Ap
20	15	75.0	1980	4 US-09-252-991A-6369	Sequence 6369, Ap
21	15	75.0	2499	4 US-09-252-991A-6182	Sequence 6182, Ap
22	15	75.0	4403765	3 US-09-103-840A-2	Sequence 2, Appl
23	15	75.0	4411529	4 US-09-103-840A-1	Sequence 1, Appl
24	14	70.0	396	4 US-09-252-991A-6707	Sequence 6707, Ap
25	14	70.0	541	4 US-09-743-207-13	Sequence 13, Appl
26	14	70.0	738	4 US-09-252-991A-2237	Sequence 2237, Ap
27	14	70.0	885	4 US-09-252-991A-10382	Sequence 10382, A

C 28	14	70.0	1206	4 US-09-489-039A-4798	Sequence 4798, Ap
C 29	14	70.0	1260	4 US-09-252-991A-6674	Sequence 6674, Ap
C 30	14	70.0	1717	4 US-09-673-395A-11	Sequence 11, Appl
C 31	14	70.0	1734	4 US-09-252-991A-2607	Sequence 2607, Ap
C 32	14	70.0	2016	4 US-09-252-991A-2445	Sequence 2445, Ap
C 33	14	70.0	2141	4 US-09-620-312D-635	Sequence 635, Ap
C 34	14	70.0	2163	4 US-09-252-991A-6641	Sequence 6641, Ap
C 35	14	70.0	2169	4 US-09-252-991A-10268	Sequence 10268, A
C 36	14	70.0	2637	4 US-09-735-934A-1	Sequence 1, Appl
C 37	14	70.0	2637	4 US-10-060-332-1	Sequence 1, Appl
C 38	14	70.0	3437	4 US-08-450-962-3	Sequence 3, Appl
C 39	14	70.0	3437	4 US-08-848-631-3	Sequence 3, Appl
C 40	14	70.0	8906	2 US-08-826-267-1	Sequence 1, Appl
C 41	14	70.0	17138	3 US-09-813-819-3	Sequence 3, Appl
C 42	14	70.0	17138	4 US-09-920-048-3	Sequence 3, Appl
C 43	14	70.0	43950	4 US-09-735-934A-3	Sequence 3, Appl
C 44	14	70.0	43950	4 US-10-060-332-3	Sequence 3, Appl
C 45	13	65.0	20	4 US-09-302-681-91	Sequence 91, Appl

#### ALIGNMENTS

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RESULT 1
US-09-726-774-11
Sequence 11, Application US/09726774
Patent No. 6677153
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Antisense Antibacterial Method and
FILE REFERENCE: 0450-0032.30
CURRENT APPLICATION NUMBER: US/09/726,774
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: US 60/168,150
NUMBER OF SEQ ID NOS: 139
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1548
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-726-774-11

Query Match      100.0%; Score 20; DB 4; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAGGAGGCGGAGATGACG 20
DB      1179 GGAGGAGGCGGAGATGACG 1198

RESULT 2
US-09-052-333A-6
Sequence 6, Application US/09052333A
Patent No. 6261769
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
Patent No. 6261769
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
STATE: IL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,333A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ribando, Curtis P.  
REGISTRATION NUMBER: 27,976  
REFERENCE/DOCKET NUMBER: 0211.97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 309/681-6513  
TELEFAX: 309/681-6688  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2751 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: rRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Chlamydia psittaci  
STRAIN: NJ1  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 1..564  
OTHER INFORMATION: /note= "16S rRNA"  
FEATURE:  
NAME/KEY: misc RNA  
LOCATION: 565..788  
OTHER INFORMATION: /note= "intergenic spacer"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 789..1409  
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 789..2751  
OTHER INFORMATION: /note= "23S rRNA"  
FEATURE:  
NAME/KEY: misc RNA  
LOCATION: 346..881  
OTHER INFORMATION: /note= "Region A - Region of the  
OTHER INFORMATION: Intergenic Spacer"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 1303..1432  
OTHER INFORMATION: /note= "Region B - The 3' End of  
OTHER INFORMATION: Domain I in the 23S rRNA"  
US-09-052-333A-6  
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Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0;  
QY 1 GGAGGAGGCGGAGATGACG 20  
DB 193 GGAGGAGGCGGAGATGACG 212  
RESULT 3  
US-09-052-333A-37  
Sequence 37, Application US/09052333A  
Patent No. 6261769  
GENERAL INFORMATION:  
APPLICANT: Everett, Karin D.E.  
APPLICANT: Andersen, Arthur A.  
TITLE OF INVENTION: Intergenic Spacer Target Sequence for  
OF INVENTION: Detecting and Distinguishing Chlamydial Strains

NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis P. Ribando  
STREET: 1815 N. University Street  
CITY: Peoria  
STATE: IL  
COUNTRY: US  
ZIP: 61604  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,333A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ribando, Curtis P.  
REGISTRATION NUMBER: 27,976  
REFERENCE/DOCKET NUMBER: 0211.97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 309/681-6513  
TELEFAX: 309/681-6688  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2762 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: rRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Chlamydia trachomatis  
STRAIN: R22  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 1..564  
OTHER INFORMATION: /note= "16S rRNA"  
FEATURE:  
NAME/KEY: misc RNA  
LOCATION: 565..802  
OTHER INFORMATION: /note= "intergenic spacer"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 803..1424  
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 803..2762  
OTHER INFORMATION: /note= "23S rRNA"  
FEATURE:  
NAME/KEY: misc RNA  
LOCATION: 346..895  
OTHER INFORMATION: /note= "Region A - Region of the  
OTHER INFORMATION: Intergenic Spacer"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 1320..1447  
OTHER INFORMATION: /note= "Region B - The 3' End of  
OTHER INFORMATION: Domain I in the 23S rRNA"  
US-09-052-333A-37  
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Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0;  
QY 1 GGAGGAGGCGGAGATGACG 20  
DB 193 GGAGGAGGCGGAGATGACG 212

ZIP: 94608  
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/01574  
FILING DATE: 19910507  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 489,676  
FILING DATE: 07-MAR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaster, Kevin R.  
REGISTRATION NUMBER: 32,704  
REFERENCE/DOCKET NUMBER: 2536.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 420-3444  
TELEFAX: (415) 658-5239  
TELEX: 4992659  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 505 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: unsure  
LOCATION: complement (35..36)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: complement (41)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: complement (67)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: complement (164..165)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: complement (167)  
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NAME/KEY: unsure  
LOCATION: complement (169)  
PCT-US91-01574-1

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Best Local Similarity 100.0%; Pred. No. 4e-05;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGAGCCGAGACGTATTCA 22  
DB 396 ACAGAGCCGAGACGTATTCA 375

RESULT 5  
US-09-052-333A-26/c  
Sequence 26, Application US/09052333A  
Patent No. 6261769  
GENERAL INFORMATION:  
APPLICANT: Everett, Karin D.E.  
APPLICANT: Andersen, Arthur A.  
TITLE OF INVENTION: Intergenic Spacer Target Sequence for  
Patent No. 6261769  
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis P. Ribando  
STREET: 1815 N. University Street

CITY: Peoria  
STATE: IL  
COUNTRY: US  
ZIP: 61604  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,333A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ribando, Curtis P.  
REGISTRATION NUMBER: 27,976  
REFERENCE/DOCKET NUMBER: 0211.97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 309/681-6513  
TELEFAX: 309/681-6688  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1284 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: rRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Chlamydia pneumoniae  
STRAIN: CWL-029  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 1..221  
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FEATURE:  
NAME/KEY: misc RNA  
LOCATION: 222..444  
OTHER INFORMATION: /note= "intergenic spacer"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 445..1063  
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 445..1284  
OTHER INFORMATION: /note= "23S rRNA"  
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NAME/KEY: misc RNA  
LOCATION: 1..537  
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OTHER INFORMATION: Intergenic Spacer"  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 959..1086  
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OTHER INFORMATION: Domain I in the 23S rRNA"  
US-09-052-333A-26

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Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGAGCCGAGACGTATTCA 22  
DB 67 ACAGAGCCGAGACGTATTCA 46

RESULT 6  
US-09-052-333A-27/c  
Sequence 27, Application US/09052333A  
Patent No. 6261769

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 919.446 Seconds

(without alignments)  
989,948 Million cell updates/sec

Title: US-09-940-860-4

Sequence: 1 gtrgcagcagcagcggtacata 21

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Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pin:\*

35: em\_hcg\_rtd:\*

36: em\_hcg\_mam:\*

37: em\_hcg\_vrt:\*

38: em\_sy:\*

39: em\_hcg\_hum:\*

40: em\_hcg\_mus:\*

41: em\_hcg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	410	1	AF128731	AF128731 Unculture
2	21	100.0	420	1	AF128692	AF128692 Unculture
3	21	100.0	434	1	AF247784	AF247784 Soil Clon
4	21	100.0	440	1	AF128656	AF128656 Unculture
5	21	100.0	495	8	AF442311	AF442311 Tetrapi
6	21	100.0	500	1	AF280951	AF280951 Unculture
7	21	100.0	508	1	AF193254	AF193254 Unculture
8	21	100.0	517	1	AF193029	AF193029 Unculture
9	21	100.0	525	1	AF193103	AF193103 Unculture
10	21	100.0	529	3	AF293558	AF293558 Unculture
11	21	100.0	534	8	AF442312	AF442312 Tetrapi
12	21	100.0	550	1	AF128705	AF128705 Unculture
13	21	100.0	552	8	AF442310	AF442310 Tetrapi
14	21	100.0	559	1	AF037640	AF037640 Unculture
15	21	100.0	564	1	AF193243	AF193243 Unculture
16	21	100.0	572	1	AF037568	AF037568 Unculture
17	21	100.0	575	1	AF037566	AF037566 Unculture
18	21	100.0	585	1	AF432842	AF432842 Tetrapi
19	21	100.0	600	8	AF442309	AF442309 Tetrapi
20	21	100.0	620	1	AF242747	AF242747 Unculture
21	21	100.0	620	1	AF242748	AF242748 Unculture
22	21	100.0	621	1	AF037626	AF037626 Unculture
23	21	100.0	648	3	AF293557	AF293557 Unculture
24	21	100.0	650	1	AF037620	AF037620 Unculture
25	21	100.0	670	1	AF193253	AF193253 Unculture
26	21	100.0	702	1	AF469392	AF469392 Unculture
27	21	100.0	756	1	AF245484	AF245484 Unculture
28	21	100.0	766	1	AF193246	AF193246 Unculture
29	21	100.0	771	1	AF469403	AF469403 Unculture
30	21	100.0	784	1	AF469398	AF469398 Unculture
31	21	100.0	796	1	AF245486	AF245486 Unculture
32	21	100.0	824	1	AF469407	AF469407 Unculture
33	21	100.0	935	3	PFAMTSST	PFAMTSST Unculture
34	21	100.0	939	3	AF040972	AF040972 Unculture
35	21	100.0	949	3	AF040974	AF040974 Plasmodu
36	21	100.0	956	1	GS16S059	GS16S059 Gordonia sp
37	21	100.0	961	3	AF040968	AF040968 Babesia b
38	21	100.0	991	1	AF172925	AF172925 Unculture
39	21	100.0	991	1	AF172926	AF172926 Unculture
40	21	100.0	991	1	AF193166	AF193166 Unculture
41	21	100.0	995	1	AF172927	AF172927 Unculture
42	21	100.0	998	3	AF040976	AF040976 Eimeria m
43	21	100.0	1013	3	AF040975	AF040975 Unculture
44	21	100.0	1023	1	AF193167	AF193167 Unculture
45	21	100.0	1024	1	AF193190	AF193190 Unculture

## ALIGNMENTS

RESULT 1

AF128731

LOCUS AF128731 410 bp DNA linear BCT 10-MAY-1999

DEFINITION Uncultured soil bacterium C065 16S ribosomal RNA, partial sequence.

ACCESSION AF128731

VERSION AF128731.1 GI:4761945

KEYWORDS

SOURCE

ORGANISM

uncultured soil bacterium C065

Bacteria; environmental samples.

REFERENCE

Dunbar,J., Takala,S., Barnes,S.M., Davis,J.A. and Kuske,C.R.

Levels of bacterial community diversity in four acid soils compared

by cultivation and 16S rRNA gene cloning in four acid soils compared

Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)

JOURNAL

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MEDLINE      99203125
PUBMED       10103265
REFERENCE    2 (bases 1 to 410)
AUTHORS      Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE        Direct Submission
JOURNAL      Submitted (15-FEB-1999) Environmental Molecular Biology, Life
              Sciences Division, Los Alamos National Laboratory, M888, Los
              Alamos, NM 87545, USA
FEATURES
  source      Location/Qualifiers
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               /clone="C065"
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               /product="16S ribosomal RNA"

ORIGIN
Query Match      100.0%; Score 21; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GTGCCAGCAGCAGCGGTATA 21
171 GTGCCAGCAGCAGCGGTATA 191

RESULT 2
LOCUS      AF128692              420 bp      DNA              linear      BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium S079 16S ribosomal RNA, partial sequence.
ACCESSION  AF128692
VERSION     AF128692.1 GI:4761906
KEYWORDS
SOURCE      unclutred soil bacterium S079
              Bacteria; environmental samples.
              1 (bases 1 to 420)
REFERENCE    Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
              Levels of bacterial community diversity in four arid soils compared
              by cultivation and 16S rRNA gene cloning
              Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL      99203125
MEDLINE     10103265
PUBMED      2 (bases 1 to 420)
AUTHORS      Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE        Direct Submission
JOURNAL      Submitted (15-FEB-1999) Environmental Molecular Biology, Life
              Sciences Division, Los Alamos National Laboratory, M888, Los
              Alamos, NM 87545, USA
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GTGCCAGCAGCAGCGGTATA 21
202 GTGCCAGCAGCAGCGGTATA 222

RESULT 3
LOCUS      AF247784              434 bp      DNA              linear      BCT 08-SEP-2000
DEFINITION Soil clone WDS 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF247784
VERSION     AF247784.2 GI:9994208
KEYWORDS
SOURCE      soil clone WDS
              Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
              Sphingomonadaceae; environmental samples.
              1 (bases 1 to 434)
REFERENCE    Dejonghe,W., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
              Verstraete,W. and Top,E.M.
              Effect of dissemination of 2,4-dichlorophenoxyacetic acid (2,4-D)
              degradation plasmids on 2,4-D degradation and on bacterial
              community structure in two different soil horizons
              Appl. Environ. Microbiol. 66 (8), 3297-3304 (2000)
JOURNAL      10919784
MEDLINE     10919784
PUBMED      2 (bases 1 to 434)
AUTHORS      Dejonghe,W.L., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
              Verstraete,W. and Top,E.M.
TITLE        Direct Submission
JOURNAL      Submitted (23-MAR-2000) Faculty of Agricultural and Applied
              Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
              Belgium
              3 (bases 1 to 434)
              Dejonghe,W.L., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
              Verstraete,W. and Top,E.M.
              Direct Submission
              Submitted (08-SEP-2000) Faculty of Agricultural and Applied
              Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
              Belgium
              Sequence update by submitter
              On Sep 8, 2000 this sequence version replaced gi:9864056.
              Location/Qualifiers
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               /organism="soil clone WDS"
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               /db_xref="taxon:135645"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GTGCCAGCAGCAGCGGTATA 21
413 GTGCCAGCAGCAGCGGTATA 433

RESULT 4
LOCUS      AF128656              440 bp      DNA              linear      BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium C0108 16S ribosomal RNA, partial
              sequence.
ACCESSION  AF128656
VERSION     AF128656.1 GI:4761870
KEYWORDS
SOURCE      unclutred soil bacterium C0108
              Bacteria; environmental samples.
              1 (bases 1 to 440)
REFERENCE    Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
              Levels of bacterial community diversity in four arid soils compared
              by cultivation and 16S rRNA gene cloning
              Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL      99203125
MEDLINE     10103265
PUBMED      2 (bases 1 to 440)
AUTHORS      Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE        Direct Submission
JOURNAL      Submitted (15-FEB-1999) Environmental Molecular Biology, Life

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